

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, Yi
- (ii) TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
 - (B) STREET: 6 Becker Farm Road
 - (C) CITY: Roseland
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/466,343
 - (B) FILING DATE: 6 JUN 1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: MULLINS, J.G.
 - (B) REGISTRATION NUMBER: 33,073
 - (C) REFERENCE/DOCKET NUMBER: 325800-449
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
 - (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1414 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAGATGGT GCTTTCATGA ATTCCTCCCA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60

GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120

TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180
 GCATTTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTATA 240
 TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
 ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
 ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
 GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
 AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
 GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
 GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr
 TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
 Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr
 ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675
 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
 AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723
 Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
 GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771
 Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
 GAA GGT CTT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT 819
 Glu Gly Leu His Tyr Thr cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
 CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867
 Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
 GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA 915
 Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
 ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG 963
 Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
 CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC 1011
 Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
 AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT 1059
 Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
 AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG 1107
 Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
 ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT 1155
 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
 GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC 1203
 Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His

ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT 1251
Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala

CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA 1299
Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu

ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG 1354
Ile Ser Val Gly Leu

TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCCTTTT 1414

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: AMINO ACIDS

(B) TYPE: AMINO ACID

(C) STRANDEDNESS:

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr
5 10 15
Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala
20 25 30
Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe
35 40 45
Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg
50 55 60
Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
65 70 75
Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala
80 85 90
Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly
95 100 105
Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln
110 115 120
Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
125 130 135
Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val
140 145 150

B' ant.

Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile
 155 160 165
 Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr cys Ser Ser
 170 175 180
 His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr
 185 190 195
 Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met
 200 205 210
 Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg
 215 220 225
 Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
 230 235 240
 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu
 245 250 255
 Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser
 260 265 270
 Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu
 275 280 285
 Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val
 290 295 300
 Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
 305 310 315
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu
 320 325 330
 Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
 335 340 345
 Gln Glu Ile Ser Val Gly Leu
 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
CGGAATTCCT CCATGGATTA TCAAGTGTC A 30

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 29 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
CGGAAGCTTC GTCACAAGCC CACAGATAT 29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 34 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
GTCCAAGCTT GCCACCATGG ATTATCAAGT GTCA 34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 61 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCACAAGCCC ACAGATATTT 60

C 61

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS

-49-

Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val
 80 85 90
 Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile
 95 100 105
 Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp
 110 115 120
 Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg
 125 130 135
 Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val
 140 145 150
 Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln
 155 160 165
 Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly
 170 175 180
 Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val
 185 190 195
 Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
 200 205 210
 Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val
 215 220 225
 Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr
 230 235 240
 Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 245 250 255
 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr
 260 265 270
 Gln Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro
 275 280 285
 Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His
 290 295 300
 Ile Ala Leu Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys
 305 310 315
 Gly Gly Pro Gly Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr
 320 325 330
 Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly Lys Ser Ile Gly
 335 340

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